

The Role of Electronic biology in double Helical Structure of DNA

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Description

The crucial discovery of double helical structure of DNA by Watson and Crick in 1953 has brought had led to the beginning of Molecular Biology Field. Further discovery of central dogma by Francis Crick in 1958 brought much more attention to the filed. In 1970s, molecular biology scientists started linking the filed with other disciplines like genetics. Other milestone discoveries of the field are Genetic information id carried by DNA in 1944, DNA polymerase discovery in 1957, DNA denaturation in 1961, DNA isolation in 1869, DNA cloning in 1972, DNA sequencing techniques in 1975 and PCR development in 1985.

Molecular Biology

Advances in the field of Molecular Biology have enabled Life Science scientists to perform experiments and investigate characteristics of genes and proteins. Since 40 years, it has had great impact on all disciplines of Life Science. Now the molecular Biology techniques can be applied to interdisciplinary studies too. This has become possible due to technical advancements and several scientific discoveries in the field. The development of software tools further enabled to store the genomic and proteomic data in-silico and analyze molecular level data. This has changed the scenario of conducting research experiments not just in Molecular Biology but also in several other subject fields such as genetics, biochemistry, biophysics, cell biology and biotechnology. Examples include Next generation sequencing and recombinant DNA technology with which we can now understand genome, gene expression, DNA repair, DNA replication, regulatory pathways at complex level.

In Biomedical scenario, personalized medicine and drug discovery investigations also have Molecular Biology relevance. In last 20 years, biomedical research has just shifted from basic study of disease in patients and organs to molecular and cellular level now. This has become possible with the advent of newer and remarkable technologies that enabled isolation and sequencing of genes, understanding gene function, within short time, Molecular Biology field has evolved to the extent that studies of human pathology are now being conducted at the molecular

level. Examples include Characterization of monogenic diseases, Cancer study at molecular and cellular level etc. Now the current knowledge of molecular biology is enough to develop efficient diagnostics and therapies in years to come.

Molecular Biology Techniques

Various molecular Biology techniques have been developed through extensive research and investigations for identification, isolation and manipulation of molecular components of cell viz., DNS, RNA and protein. These techniques include Molecular mapping, molecular cloning, Microarrays, Molecular probing and blotting, Gene delivery, DNA sequencing, Gel electrophoresis, Polymerase Chain Reaction (PCR) etc. Applications of Molecular Biology have been observed in Research, Diagnosis, Paternity testing, Pedigree verification, Forensic analysis, Gene therapy, Drig design and Genotyping. Bioinformatics filed emerged and taken genetic and proteomic analysis to the in-silico level. Much software has been developed to analyses and modifies DNA sequence. These software suites offer various different features like SNP analysis, miRNA analysis, genome and transcriptase assembly and analysis, Thus, Molecular Biology field is ever developing for much more research investigations to be possible in Life Science disciplines.

By misusing the capacity of *Pseudomonas aeruginosa* to contaminate a assortment of vertebrate and non-vertebrate has, we have created demonstrate frameworks that utilize plants and nematodes as adjuncts to mammalian models to assist illustrate the atomic premise of *P. aeruginosa* pathogenesis. Our studies uncover a surprising degree of preservation within the destructiveness instruments utilized by *P. aeruginosa* to contaminate has of unique developmental roots. Bacterial pathogens taint a wide assortment of developmental unmistakable has, counting both lower and higher eukaryotes. In all of these cases, the pathogen must have the capacity to recognize, gotten to be related with, misuse the supplement saves of, and combat the defense reactions of its particular have. To achieve these assignments, pathogens utilize a broad weapons store of virulence-related components. Numerous pathogens cause infection in a single or restricted number of has species as a result of a long evolutionary history. In any case, the intelligent between have and pathogen that

restrain have extend and decide have resistance or helplessness are ineffectively caught on. In spite of the fact that numerous bacterial harmfulness components are thought to be host-specific, various ponders have illustrated the presence of what show up to be all inclusive harmfulness instruments utilized by differing bacterial species. Essentially, later work has uncovered common highlights fundamental have defense reactions against pathogens in plants, creepy crawlies, and well evolved creatures. In this way, a few of the fundamental destructiveness instruments of pathogens, as well as the have resistances against them, are likely to have old developmental roots protected over phylogeny. There remains an incredible bargain to memorize approximately the atomic nature of opposing experiences between pathogenic microbes and In spite of our constrained information, critical propels have been made in creating strategies that encourage our understanding of harmfulness instruments and the basic part of the have amid pathogenesis. Our research facilities have created a method, which we allude to as multihost pathogenesis, to consider pathogens that cause infection in both vertebrate and nonvertebrate. Epidemiological considers carried out within the 1970s proposed that clinical isolates of *Pseudomonas aeruginosa* may well be able of causing malady in plants.

Based on this preface, we created a demonstrate pathogenesis framework by employing a human clinical disconnect of *P. aeruginosa*, strain UCBPP-PA14 (PA14) that evokes malady in plants, nematodes, creepy crawlies, and mice. *P. aeruginosa* is the foremost common causative life form of sepsis in burned patients and the driving cause of aspiratory contaminations and mortality in cystic fibrosis patients. In expansion, this vital human deft pathogen taints harmed, immunodeficient, or something else compromised people. The pathophysiology of contaminations caused by *P. aeruginosa* is complex as appeared by the clinical differing qualities of infections related with this life form and the assortment of harmfulness variables it produces. In spite of the fact that a common soil occupant, *P. aeruginosa* is flexible in its metabolic potential, which permits it to outlive in a assortment of normal and healing center situations. It shows up that the combination of natural determination, flexibility in destructiveness instruments, and different destructiveness components permits *P. aeruginosa* to be viable both as an artful human pathogen and as a plant pathogen.